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6297.1CP.ST25.txt  
SEQUENCE LISTING

<110> Lowery, David E.  
Smith, Valdin G.  
Kubiak, Teresa M.  
Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods Related To The Same

<130> 6297.1cp

<140> 09/693,746  
<141> 2000-10-20

<150> 09/425,676  
<151> 1999-10-22

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Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg  
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Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr  
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly  
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg  
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Gln Leu Ile Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr  
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Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly  
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Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile  
100 105 110

Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp  
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Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile  
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260 265 270

Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile  
275 280 285

Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg  
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Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala  
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Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys  
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Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly  
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Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Leu  
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Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr  
165 170 175

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290 295 300

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aatcacagcc agaccctatac caccgaccag cccgcccgtcg gggacgtgga agacgcggcc 240  
gaggatgcgg cggcgccat ggagacgggc tcgtttgcat ttgtggtccc gtggtggcgt 300  
caggtgctct ggagcatcct ctccggcggc atggtcattt tggcgacggg cgtaacactg 360  
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gcgatgctaa gcatctgcgc ctcagtgttc accctaattgg ccatctccat cgacagatac 600  
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6297.1CP.ST25.txt

<210> 10  
<211> 519  
<212> PRT  
<213> D. melanogaster

<400> 10

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Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser  
20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp  
35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln  
50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala  
65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val  
85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val  
100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr  
115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser  
130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr  
145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu  
165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu  
180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln  
195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Val Ile Trp  
210 215 220

## 6297.1CP.ST25.txt

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr  
 225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro  
 245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr  
 260 265 270

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met  
 275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr  
 290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg  
 305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys  
 325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala  
 340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp  
 355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met  
 370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu  
 385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr  
 405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg  
 420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys  
 435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg  
 450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly  
 465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp

6297.1CP.ST25.txt

485

490

495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Thr Ala  
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Asn Thr Thr Gln Leu Leu Ser  
515

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<211> 1568  
<212> DNA  
<213> *D. melanogaster*

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ctctcgccca gcaaccatac gcctctgccg gactttggcc aggagctcgc cctatccacc 180  
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gacgcggccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtccc 300  
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cagttcatcg cgatgctaag catctgcgcc tcagtgttca ccctaattggc catctccatc 600  
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gccatcgccg cggcatctg gctggccctcc acgctcatct cctggcccat gatgatcatc 720  
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tggcccgatg ggccccaccaa tcactccacg atggaggcccc tctacaacat cctcatcatc 840  
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gagctctggg gatccaagac catcgccgag tgacacgcccc gccaggtggaa gaatgtgcgg 960  
agtaagcgaa gggtggtgaa gatgatgatt gtggcgtcc tgatattcgac catcgctgg 1020  
ctgcccgttcc acagctactt cataatcaca tcctgttacc cggccatcac ggaggcgccc 1080  
ttcatccagg aactttaccc ggcacatctac tggctggcca tgagcaactc catgtacaat 1140  
cccattatat actgctggat gaattcgccgc tttcgctatg gtttcaagat ggtcttccgc 1200  
tggtgccctgt ttgtgcgcgt gggcactgaa cccttagtc ggcggggagaa cctgacatcc 1260  
cggtactcct gctccgggttc cccggatcac aatcgcatca agcgcaatga taccagaaaa 1320  
tcgatacttt atacctgtcc cagctcaccc aagtgcgcattc gaatttcgca cagcggaaaca 1380  
ggtcgcagtg cgacgcgttagt gaaacagtctg ccggccggagt cattgtcgcc cggtggatct 1440

6297.1CP.ST25.txt

ggaggtggag gacacaggaa acggttgtcc taccaggagg aaatgcagca gcgggtggta	1500
ggacccaata gtgccaccgc agtgaccaat tccagcagta cggccaacac cacccaaactg	1560
ctctccctg	1568
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<211> 522	
<212> PRT	
<213> D. melanogaster	
<400> 12	
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Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val	
20                         25                         30	
Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro	
35                         40                         45	
Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn	
50                         55                         60	
His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu	
65                         70                         75                         80	
Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala	
85                         90                         95	
Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly	
100                         105                         110	
Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile	
115                         120                         125	
Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val	
130                         135                         140	
Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe	
145                         150                         155                         160	
Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr	
165                         170                         175	
Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val	
180                         185                         190	
Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg	
195                         200                         205	

6297.1CP.ST25.txt

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala  
210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile  
225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val  
245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu  
260 265 270

Ser Leu Tyr Asn Ile Leu Ile Ile Leu Thr Tyr Phe Leu Pro Ile  
275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly  
290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg  
305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe  
325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys  
340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala  
355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr  
370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg  
385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu  
405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg  
420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser  
435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala  
450 455 460

## 6297.1CP.ST25.txt

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser  
 465 470 475 480

Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln  
 485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser  
 500 505 510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser  
 515 520

<210> 13  
 <211> 1394  
 <212> DNA  
 <213> D. melanogaster

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ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc	180
aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc	240
actgtgatga tgaactttag ctgtgacgac tatgaccttc tatcgagga catgtggtct	300
agtgcctact ttaagatcat cgtctacatg ctctacattc ccattttat ctgcgcctg	360
atcggcaacg gaacggtctg ctatatcgctc tattccacac ctcgcattgcg cacggtcacc	420
aattacttta tagccagctt gccatcggc gacatctga tgtccttctt ctgcgttccg	480
tctcgcttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac	540
tttgtgaact actcgaggc ggtctcagtt ctggcagcg cctatacttt ggtggcaatt	600
agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcattcac aaaacgctat	660
gccaccttca tcatcgccgg cgtttggtt attgcacttg ccacccgact tcccataccc	720
atcgctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgcga gaaatacatt	780
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gtctggcga aacgaccgccc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc	960
tccaaacgga agatggtaa aatgatgctg acgggtgtga ttgtgttcac ctgctgtgg	1020
ctgcaccccttca atattttgcg gctttactg aacgacgagg agttcgccca ctggatcct	1080
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atgcccggcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact	1260
tccggAACGG gtccagcact tcctctcaat cgaatgaaca catccaccac ctacatcagc	1320

## 6297.1CP.ST25.txt

gctcgtcgaa agccacgagc gacatcttg cgagcgaacc cattatcatg cggcgagacg 1380  
 tcaccactgc ggta 1394

<210> 14  
 <211> 464  
 <212> PRT  
 <213> D. melanogaster  
 <400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met  
 1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
 20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
 35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
 50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
 65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
 85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
 100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr  
 115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu  
 165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
 195 200 205

## 6297.1CP.ST25.txt

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile  
 210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro  
 225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys  
 245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr  
 260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly  
 275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys  
 290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg  
 305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe  
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp  
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe  
 355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys  
 370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg  
 385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg  
 405 410 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met  
 420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr  
 435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg  
 450 455 460

## 6297.1CP.ST25.txt

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<212> DNA  
<213> D. melanogaster

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ccggaccctg catccttaact ttacaataacc accgcactgc cagcggacga tgaagggtcc	180
aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc	240
actgtgatga tgaacttagt ctgtgacgac tatgaccttc tatcggagga catgtggtct	300
agtgcctact ttaagatcat cgtctacatg ctctacatttccatctttat ctgcgcctg	360
atcgcaacg gaacggctcg ctatatcgtc tattccacac ctgcgcacgac cacggtcacc	420
aattacttta tagccagctt ggccatcgcc gacatcctga tgtccttctt ctgcgtccg	480
tcgtccttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac	540
tttgtgaact actcgaggc ggtctcagtt ctggcagcg cctataacttt ggtggcaatt	600
agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcacacaaaacgctat	660
gccaccttca tcatcgccgg cgtttggtt attgcacttg ccacccgact tcccatacc	720
atcgctctcg gactcgacat cccaatgtcg ccgtggcaca cggaaatgcga gaaatacatt	780
tgcgcgaaaa tgtggccgtc gcggacgcag gagtactact acaccctgtc cctcttcgc	840
ctgcagttcg tcgtgcccgtc gggcgtgctc atcttcaccc acggccggat caccatcgc	900
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tccaaacgga agatggtcaa aatgatgctg acggtgtga ttgtgttacatgtgttgg	1020
ctgcccattca atattttgca gcttttactg aacgacgagg agttcgccca ctggatcct	1080
ctgcccgtatg tgtggttcgc gtttcaactgg ctggccatgt cgactgtctgtatcc	1140
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tccggtgaga tgactacgaa gtaccatcgccatgtcgatggcatttccggaaaccc	1320
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ctacatcagc gctcgtaaa agccacgagc gacatcttgcgagcacc cattatcatg	1440
cgccgagacg tcaccactgc ggtagctgtc atatcaaaaa ataaaaactga ttccaccggtg	1500
cgccgatcgg gaagctcagg tgaaacagaa gcaaacataa gaagcaccga gttttg	1556

<210> 16  
<211> 518  
<212> PRT  
<213> D. melanogaster

<400> 16

## 6297.1CP.ST25.txt

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 1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
 20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
 35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
 50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
 65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
 85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
 100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr  
 115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu  
 165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
 195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile  
 210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro  
 225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys  
 245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr

## 6297.1CP.ST25.txt

260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly  
275 280 285Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys  
290 295 300Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg  
305 310 315 320Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe  
325 330 335Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Asn Asp  
340 345 350Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe  
355 360 365His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys  
370 375 380Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg  
385 390 395 400Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg  
405 410 415Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val  
420 425 430Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser  
435 440 445Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg  
450 455 460Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met  
465 470 475 480Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr  
485 490 495Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn  
500 505 510Ile Arg Ser Thr Glu Phe  
515

<210> 17  
 <211> 1628  
 <212> DNA  
 <213> D. melanogaster

<400> 17						
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gaagcagaat	ttgagcgtct	atacgccgt	cccgctgaga	tttgtggccct	gttgtccatt	120
ttctatgggg	gaatcagtat	cgtggccgtc	attggcaaca	cttgggtcat	ctgggtggtg	180
gccacgacca	ggcaaatgcg	gaccgtgaca	aatatgtata	tcgctaattt	ggctttgcc	240
gatgtgatta	ttggcctctt	ctgcataccca	tttcagttcc	aggctgccct	gctgcagagt	300
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gaacaggaat	ttggcagcca	aaccgaatgc	gatggcacct	gcataactcag	cgaggtgtcg	1560
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## 6297.1CP.ST25.txt

<210> 18  
<211> 542  
<212> PRT  
<213> D. melanogaster

<400> 18

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Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala  
20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val  
35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg  
50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala  
65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala  
85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro  
100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala  
115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg  
130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu  
145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu  
165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg  
180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe  
195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile  
210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala  
225 230 235 240

6297.1CP.ST25.txt

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys  
245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu  
260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro  
275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp  
290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile  
305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys  
325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser  
340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser  
355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn  
370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala  
385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn  
405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro  
420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg  
435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp  
450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu  
465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser  
485 490 495

## 6297.1CP.ST25.txt

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly  
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Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln  
 515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu  
 530 535 540

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<211> 1451  
<212> DNA  
<213> D. melanogaster

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aaccatagat ggatttagtgg tagttccaca attcagccag aggagtccct ttatggcact	180
gatttgccca cctatcaaca ttgcatagcc acgcggaatt cctttgctga cttgttca	240
gtggtgctct acggatttgt gtgcattatc ggattatttgc gcaacaccct ggtgatctac	300
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gtggcagacg agtgcttcct gatttggaaata cccttctgc tgtacacaat gcgaatttgc	420
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ccgatttcct cgccacgata tcgaactctg catattgcca aagtggtctc agcgattgcc	600
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gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg	720
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cggaaagagct tcttcaaggc cttaacgtt atgaataagc aggatataa cgctcaactc	1140
cagctggagc ccagtgtttt caccaaacag ggcagtaaaa agaggggtgg ctccaagcgc	1200
ctgttgcacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat	1260
tcatcgacca ccacatccctc gaccacgaca gcggaaaaga ccggaaccac gggacacag	1320
aaatcatgca attccaatgg caaagtgaca gctccgcccgg agaatttgat tataatgttt	1380

6297.1CP.ST25.txt

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<213>	D. melanogaster					
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20	25		30			
Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser						
35	40		45			
Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr						
50	55		60			
Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr						
65	70		75		80	
Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr						
85	90		95			
Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr						
100	105		110			
Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile						
115	120		125			
Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe						
130	135		140			
Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser						
145	150		155		160	
Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile						
165	170		175			
Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile						
180	185		190			
Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met						
195	200		205			
Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile						

## 6297.1CP.ST25.txt

210	215	220
Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser		
225	230	235
240		
Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro		
245	250	255
Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg		
260	265	270
270		
Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala		
275	280	285
His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile		
290	295	300
Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser		
305	310	315
320		
Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu		
325	330	335
Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu		
340	345	350
Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe		
355	360	365
Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro		
370	375	380
Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg		
385	390	395
400		
Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala		
405	410	415
Gly Asn Asn Asn Ser Ser Thr Thr Ser Ser Thr Thr Thr Ala Glu		
420	425	430
Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys		
435	440	445
Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln		
450	455	460
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Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln		
470	475	480

Thr Asp Leu

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<211> 1754  
<212> DNA  
<213> D. melanogaster

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aacgtggcac cctacaatgg aactggaaac ggaggcactg ttccttggc gggcaatgcg	180
acaaggcagct atggcgatga tgatagggat ggctatatgg acaccgagcc cagtgacctg	240
gtcaccgaac tggcctctc cctggcaccc agttcaagtc caagtcccag ttccacaccc	300
gcttccagct ccagtaacttc cactggcatg cccgtctggc tgatacccaag ctatagcatg	360
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cgtaccctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgctgcct	960
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accttcaagg gtctgcccgt gcgtcgtgga gcaggtgcca gcggaggcgt cggtggtgct	1560
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## 6297.1CP.ST25.txt

aacaccaaca	ttagtctcaa	tcccgcccta	gccatggta	tgggcacctg	gcggagtcgc	1680
tcacgccacg	agtttctcaa	tgcggtggtg	accaccaata	gtgccgcccgc	cggcgtcaac	1740
agtccctcagc	tctaa					1754

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<211> 584  
<212> PRT  
<213> D. melanogaster

&lt;400&gt; 22

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Ala	Ala	Ala	Tyr	Arg	Ala	Leu	Leu	Asp	Tyr	Tyr	Ala	Asn	Ala	Pro	Ser
				20			25						30		

Ala	Ala	Gly	His	Ile	Val	Ser	Leu	Asn	Val	Ala	Pro	Tyr	Asn	Gly	Thr
				35			40					45			

Gly	Asn	Gly	Gly	Thr	Val	Ser	Leu	Ala	Gly	Asn	Ala	Thr	Ser	Ser	Tyr
				50			55					60			

Gly	Asp	Asp	Asp	Arg	Asp	Gly	Tyr	Met	Asp	Thr	Glu	Pro	Ser	Asp	Leu
65				70				75					80		

Val	Thr	Glu	Leu	Ala	Phe	Ser	Leu	Gly	Thr	Ser	Ser	Ser	Pro	Ser	Pro
					85			90					95		

Ser	Ser	Thr	Pro	Ala	Ser	Ser	Ser	Thr	Ser	Thr	Gly	Met	Pro	Val
					100			105				110		

Trp	Leu	Ile	Pro	Ser	Tyr	Ser	Met	Ile	Leu	Leu	Phe	Ala	Val	Leu	Gly
					115			120					125		

Asn	Leu	Leu	Val	Ile	Ser	Thr	Leu	Val	Gln	Asn	Arg	Arg	Met	Arg	Thr
					130			135				140			

Ile	Thr	Asn	Val	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Met	Leu	Leu
145				150				155					160		

Gly	Val	Leu	Cys	Met	Pro	Val	Thr	Leu	Val	Gly	Thr	Leu	Leu	Arg	Asn
				165				170					175		

Phe	Ile	Phe	Gly	Glu	Phe	Leu	Cys	Lys	Leu	Phe	Gln	Phe	Ser	Gln	Ala
					180			185				190			

Ala	Ser	Val	Ala	Val	Ser	Ser	Trp	Thr	Leu	Val	Ala	Ile	Ser	Cys	Glu
					195			200				205			

6297.1CP.ST25.txt

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr  
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile  
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser  
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr  
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Val Leu Pro  
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr  
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro  
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser  
325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn  
340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly  
355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala  
370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Val Thr Leu Ala Lys  
385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser  
405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu  
420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val  
435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val  
450 455 460

## 6297.1CP.ST25.txt

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser  
 465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg  
 485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly  
 500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser  
 515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile  
 530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg  
 545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala  
 565 570 575

Ala Ala Val Asn Ser Pro Gln Leu  
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<210> 23  
 <211> 1452  
 <212> DNA  
 <213> D. melanogaster

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gagggtctgg cactggatata gggccacaat gccagcgccg acggcgaaat agtaccgtat	180
gtgcccgtgc tggaccggccc ggagacgtac attgtcaccg tgctgtacac gctcatcttc	240
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aagccgctca ctgttttac tgcgggtatg atctggatcc tggccatccct actggccatg	600
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aaggcactgg tgtactaccc tttggccgtg tccatcatttggggcgctata catcatgtatg	780

6297.1CP.ST25.txt

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atgcgctact aa	1452

<210> 24  
<211> 483  
<212> PRT  
<213> D. melanogaster  
<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu  
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Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr  
20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Glu Gly Leu Ala Leu Asp Met Gly  
35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu  
50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe  
65 70 75 80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg  
85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala  
100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile  
115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile

## 6297.1CP.ST25.txt

130	135	140
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145	150	155
Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg		
165	170	175
Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp		
180	185	190
Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile		
195	200	205
Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val		
210	215	220
Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly		
225	230	235
240		
Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu		
245	250	255
Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro		
260	265	270
Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu		
275	280	285
His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys		
290	295	300
Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr		
305	310	315
320		
Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro		
325	330	335
Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe		
340	345	350
Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln		
355	360	365
Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr		
370	375	380
Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly		
385	390	395
400		

6297.1CP.ST25.txt

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly  
405 410 415

Ala Gly Gly Val Gly Gly Val Gly Ser Gly Arg Val Gly Ser  
420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly  
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Gly Gly Ala Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr  
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Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val  
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Met Arg Tyr

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